



Dkt. #873-US *Cofe*

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant(s) : BERMUDEZ, et al.

U.S. Serial No.: 09/645,415, now U.S. Patent No. 6,962,696, *B1*
issued November 8, 2005

Filing Date : August 24, 2000

For : COMPOSITIONS AND METHODS FOR TUMOR-TARGETED
DELIVERY OF EFFECTOR MOLECULES

Law Offices of Albert Wai-Kit Chan, LLC
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March 10, 2006

Certificate

MAR 17 2006

of Correction

Certificate of Corrections Branch
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Sir/Madam:

COMMUNICATION TO REQUEST CERTIFICATE OF CORRECTION

Applicants hereby submit a request for a Certificate of Correction for the above-identified issued patent. In sum, Sequence Listing #34, beginning on column 105, line 67, and extending to column 111, line 66, of the issued patent, is missing its first column of letters. The error was not the result of Applicants' mistake, as it was correctly shown in the Sequence Listing, which was filed with the United States Patent & Trademark Office (USPTO) on January 7, 2002.

Form PTO/SB/44, which correctly shows Sequence Listing #34, is attached hereto as **Exhibit A**. A copy of the entire Sequence Listing, which was filed on January 7, 2002 and shown on the USPTO Patent Application Information Retrieval (PAIR) System, is

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Applicant(s) : BERMUDEZ, et al.
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attached hereto as **Exhibit B**. Accordingly and pursuant to 35 U.S.C. 254, Applicants respectfully request the issuance of a Certificate of Correction without charge.

If a telephone interview would be of assistance in addressing the subject matter of the present case, Applicants' undersigned attorney invites the Examiner to telephone him at the number provided below.

Pursuant to 35 U.S.C. 254, as noted *supra*, no fee is necessary in connection with the filing of this Communication. However, if any fee is required, authorization is hereby given to charge the amount of any such fee to Deposit Account No. 50-1891.

Respectfully submitted,

Albert Wai Kit Chan

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Albert Wai Kit Chan 3/10/06
Albert Wai-Kit Chan Date
Reg. No. 36,479

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CERTIFICATE OF CORRECTION

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PATENT NO. : 6,962,696 β 1
APPLICATION NO.: 09/645,415
ISSUE DATE : November 8, 2005
INVENTOR(S) : BERMUDES, et al.

It is certified that an error appears or errors appear in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

Sequence Listing 34, which begins on column 105, line 67, and extending to column 111, line 66, is missing its first column of letters and should read as follows:

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Page 2 of 4

PATENT NO. : 6,962,696 *Bi*
 APPLICATION NO.: 09/645,415
 ISSUE DATE : November 8, 2005
 INVENTOR(S) : BERMUDEZ, et al.

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Page 3 of 4

PATENT NO. : 6,962,696 *B1*
APPLICATION NO.: 09/645,415
ISSUE DATE : November 8, 2005
INVENTOR(S) : BERMUDEZ, et al.

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Page 4 of 4

PATENT NO. : 6,962,696 ^{B1}
APPLICATION NO.: 09/645,415
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INVENTOR(S) : BERMUDES, et al.

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Clairmont, C.
Lin, S.
Belcourt, M.

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 gct atc aag tct ccg tgc cag cgt gaa act ccc gag ggt gca gaa gcg 336
 Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
 100 105 110
 aaa cca tgg tat gaa ccg atc tac ctg ggt ggc gta ttt caa ctg gag 384
 Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu
 115 120 125
 aaa ggt gac cgt ctg tcc gca gaa atc aac cgt cct gac tat cta gat 432
 Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
 130 135 140
 ttc gct gaa tct ggc cag gtg tac ttc ggt att atc gca ctg 474
 Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
 145 150 155
 taa 477

<210> 4
 <211> 158
 <212> PRT
 <213> Homo sapiens

<400> 4
 Met Val Arg Ser Ser Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His
 1 5 10 15
 Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg
 20 25 30
 Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln
 35 40 45
 Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu
 50 55 60
 Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr His Thr
 65 70 75 80
 Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser
 85 90 95
 Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala
 100 105 110
 Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu
 115 120 125
 Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp
 130 135 140

Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu
 145 150 155

<210> 5
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Forward primer

<400> 5
 ccgacgcgtt gacacctgaa aactggag

28

<210> 6
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Reverse primer

<400> 6
 ccgacgcgtg aaaggatctc aagaagatc

29

<210> 7
 <211> 543
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Fusion construct

<221> CDS
 <222> (1)...(540)

<400> 7

atg aag aag aca gct atc gcg att gca gtg gca ctg gct ggt ttc gct
 Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
 1 5 10 15

48

acc gta gcg cag gcc cat atg gta cgt agc tcc tct cgc act ccg tcc
 Thr Val Ala Gln Ala His Met Val Arg Ser Ser Ser Arg Thr Pro Ser
 20 25 30

96

gat aag ccg gtt gct cat gta gtt gct aac cct cag gca gaa ggt cag
 Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln
 35 40 45

144

ctg cag tgg ctg aac cgt cgc gct aac gcc ctg ctg gca aac ggc gtt
 Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val
 50 55 60

192

gag ctc cgt gat aac cag ctc gtg gta cct tct gaa ggt ctg tac ctg
 Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu
 65 70 75 80

240

atc tat tct caa gta ctg ttc aag ggt cag ggc tgc ccg tct act cat
 Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His
 85 90 95

288

gtt ctg ctg act cac acc atc agc cgt att gct gta tct tac cag acc 336
 Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr
 100 105 110

aaa gtt aac ctg ctg agc gct atc aag tct ccg tgc cag cgt gaa act 384
 Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr
 115 120 125

ccc gag ggt gca gaa gcg aaa cca tgg tat gaa ccg atc tac ctg ggt 432
 Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly
 130 135 140

ggc gta ttt caa ctg gag aaa ggt gac cgt ctg tcc gca gaa atc aac 480
 Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn
 145 150 155 160

cgt cct gac tat cta gat ttc gct gaa tct ggc cag gtg tac ttc ggt 528
 Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly
 165 170 175

att atc gca ctg taa 543
 Ile Ile Ala Leu
 180

<210> 8
 <211> 180
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fusion construct

<400> 8

Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
 1 5 10 15
 Thr Val Ala Gln Ala His Met Val Arg Ser Ser Ser Arg Thr Pro Ser
 20 25 30
 Asp Lys Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln
 35 40 45
 Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val
 50 55 60
 Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu
 65 70 75 80
 Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His
 85 90 95
 Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr
 100 105 110
 Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr
 115 120 125
 Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly
 130 135 140
 Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn
 145 150 155 160
 Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly
 165 170 175
 Ile Ile Ala Leu
 180

<210> 9
 <211> 801
 <212> DNA

<213> Artificial Sequence

<220>

<223> Fusion construct

<221> CDS

<222> (1)...(798)

<400> 9

atg aaa aag aca gct atc gcg att gca gtg gca ctg gct ggt ttc gct 48
Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
1 5 10 15

acc gta gcg cag gcc cat atg gct aac gag ctg aag cag atg cag gac 96
Thr Val Ala Gln Ala His Met Ala Asn Glu Leu Lys Gln Met Gln Asp
20 25 30

aag tac tcc aaa agt ggc att gct tgt ttc tta aaa gaa gat gac agt 144
Lys Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser
35 40 45

tat tgg gac ccc aat gac gaa gag agt atg aac agc ccc tgc tgg caa 192
Tyr Trp Asp Pro Asn Asp Glu Ser Met Asn Ser Pro Cys Trp Gln
50 55 60

gtc aag tgg caa ctc cgt cag ctc gtt aga aag atg att ttg aga acc 240
Val Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr
65 70 75 80

tct gag gaa acc att tct aca gtt caa gaa aag caa caa aat att tct 288
Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser
85 90 95

ccc cta gtg aga gaa aga ggt cct cag aga gta gca gct cac ata act 336
Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr
100 105 110

ggg acc aga gga aga agc aac aca ttg tct tct cca aac tcc aag aat 384
Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn
115 120 125

gaa aag gct ctg ggc cgc aaa ata aac tcc tgg gaa tca tca agg agt 432
Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser
130 135 140

ggg cat tca ttc ctg agc aac ttg cac ttg agg aat ggt gaa ctg gtc 480
Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val
145 150 155 160

atc cat gaa aaa ggg ttt tac tac atc tat tcc caa aca tac ttt cga 528
Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg
165 170 175

ttt cag gag gaa ata aaa gaa aac aca aag aac gac aaa caa atg gtc 576
Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val
180 185 190

caa tat att tac aaa tac aca agt tat cct gac cct ata ttg ttg atg 624
Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met
195 200 205

aaa agt gct aga aat agt tgt tgg tct aaa gat gca gaa tat gga ctc 672
 Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu
 210 215 220
 tat tcc atc tat caa ggg gga ata ttt gag ctt aag gaa aat gac aga 720
 Tyr Ser Ile Tyr Gln Gly Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg
 225 230 235 240
 att ttt gtt tct gta aca aat gag cac ttg ata gac atg gac cat gaa 768
 Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu
 245 250 255
 gcc agt ttt ttc ggg gcc ttt tta gtt ggc taa 801
 Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
 260 265

<210> 10
 <211> 266
 <212> PRT
 <213> Artificial Sequence
 <220>
 <223> Fusion construct

<400> 10
 Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
 1 5 10 15
 Thr Val Ala Gln Ala His Met Ala Asn Glu Leu Lys Gln Met Gln Asp
 20 25 30
 Lys Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser
 35 40 45
 Tyr Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln
 50 55 60
 Val Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr
 65 70 75 80
 Ser Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser
 85 90 95
 Pro Leu Val Arg Glu Arg Gly Pro Gln Arg Val Ala Ala His Ile Thr
 100 105 110
 Gly Thr Arg Gly Arg Ser Asn Thr Leu Ser Ser Pro Asn Ser Lys Asn
 115 120 125
 Glu Lys Ala Leu Gly Arg Lys Ile Asn Ser Trp Glu Ser Ser Arg Ser
 130 135 140
 Gly His Ser Phe Leu Ser Asn Leu His Leu Arg Asn Gly Glu Leu Val
 145 150 155 160
 Ile His Glu Lys Gly Phe Tyr Tyr Ile Tyr Ser Gln Thr Tyr Phe Arg
 165 170 175
 Phe Gln Glu Glu Ile Lys Glu Asn Thr Lys Asn Asp Lys Gln Met Val
 180 185 190
 Gln Tyr Ile Tyr Lys Tyr Thr Ser Tyr Pro Asp Pro Ile Leu Leu Met
 195 200 205
 Lys Ser Ala Arg Asn Ser Cys Trp Ser Lys Asp Ala Glu Tyr Gly Leu
 210 215 220
 Tyr Ser Ile Tyr Gln Gly Ile Phe Glu Leu Lys Glu Asn Asp Arg
 225 230 235 240
 Ile Phe Val Ser Val Thr Asn Glu His Leu Ile Asp Met Asp His Glu
 245 250 255
 Ala Ser Phe Phe Gly Ala Phe Leu Val Gly
 260 265

<210> 11
 <211> 465
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Fusion construct

<221> CDS
 <222> (1)...(462)

<400> 11

atg aaa aag acg gct ctg gcg ctt ctg ctc ttg ctg tta gcg ctg act 48
 Met Lys Lys Thr Ala Leu Ala Leu Leu Leu Leu Leu Ala Leu Thr
 1 5 10 15

agt gta gcg cag gcc gct cct act agc tcg agc act aag aaa act caa 96
 Ser Val Ala Gln Ala Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln
 20 25 30

ctg caa ttg gag cat ctg ctg ctg gat ctg cag atg att ctg aat ggc 144
 Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly
 35 40 45

atc aat aac tac aag aac cct aag ctg act cgc atg ctg act ttc aaa 192
 Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys
 50 55 60

ttc tac atg ccg aaa aag gct acc gag ctc aaa cat ctc cag tgc ctg 240
 Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu
 65 70 75 80

gaa gag gaa ctg aag ccg ctg gag gaa gta ctt aac ctg gca cag tct 288
 Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser
 85 90 95

aag aac ttc cac ctg cgt ccg cgt gac ctg atc tcc aac atc aat gta 336
 Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val
 100 105 110

atc gtt ctt gag ctg aag gga tcc gaa acc acc ttc atg tgc gaa tac 384
 Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr
 115 120 125

gct gac gaa acc gcc acc att gtg gag ttc ctg aac cgt tgg atc acc 432
 Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr
 130 135 140

ttt gcc caa tgc atc att agc acg tta act taa 465
 Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
 145 150

<210> 12
 <211> 154
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Fusion construct

<400> 12
 Met Lys Lys Thr Ala Leu Ala Leu Leu Leu Leu Leu Ala Leu Thr
 1 5 10 15
 Ser Val Ala Gln Ala Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln
 20 25 30
 Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly
 35 40 45
 Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys
 50 55 60
 Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu
 65 70 75 80
 Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser
 85 90 95
 Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val
 100 105 110
 Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr
 115 120 125
 Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr
 130 135 140
 Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
 145 150

<210> 13
 <211> 465
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Fusion construct

<221> CDS
 <222> (1)...(462)

<400> 13
 atg aaa cag tcg act ctg gcg ctt ctg ctg ttg ctg tta gcg ctg act 48
 Met Lys Gln Ser Thr Leu Ala Leu Leu Leu Leu Leu Ala Leu Thr
 1 5 10 15
 --- agt gtg gcc aaa gcg gct cct act agc tcg agc act aag aaa act caa 96
 Ser Val Ala Lys Ala Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln
 20 25 30
 ctg caa ttg gag cat ctg ctg ctg gat ctg cag atg att ctg aat ggc 144
 Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly
 35 40 45
 atc aat aac tac aag aac cct aag ctg act cgc atg ctg act ttc aaa 192
 Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys
 50 55 60
 ttc tac atg ccg aaa aag gct acc gag ctg aaa cat ctg cag tgc ctg 240
 Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu
 65 70 75 80
 gaa gag gaa ctg aag ccg ctg gag gaa gta ctt aac ctg gca cag tct 288
 Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser
 85 90 95
 aag aac ttc cac ctg cgt ccg cgt gac ctg atc tcc aac atc aat gta 336
 Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val
 100 105 110

atc gtt ctt gag ctg aag gga tcc gaa acc acc ttc atg tgc gaa tac 384
 Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr
 115 120 125

gct gac gaa acc gcc acc att gtg gag ttc ctg aac cgt tgg atc acc 432
 Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr
 130 135 140

ttt gcc caa tcc atc att agc acg tta act taa 465
 Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
 145 150

<210> 14
 <211> 154
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Fusion construct

<400> 14
 Met Lys Gln Ser Thr Leu Ala Leu Leu Leu Leu Leu Ala Leu Thr
 1 5 10 15
 Ser Val Ala Lys Ala Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln
 20 25 30
 Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly
 35 40 45
 Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys
 50 55 60
 Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu
 65 70 75 80
 Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser
 85 90 95
 Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val
 100 105 110
 Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr
 115 120 125
 Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr
 130 135 140
 Phe Ala Gln Ser Ile Ile Ser Thr Leu Thr
 145 150

<210> 15
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Forward primer

<400> 15

agtctagaca atcaggcgaa gaacgg

26

<210> 16
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Reverse primer

<400> 16
agccatggag tcaccctcac ttttc 25

<210> 17
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward primer

<400> 17
ggatccttaa gaccacttt cacatttaag t 31

<210> 18
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse primer

<400> 18
ggttccatgg ttcaacttttc tctatcac 28

<210> 19
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward primer

<400> 19
gtgtccatgg ggcacagcca ccgcgacttc cag 33

<210> 20
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Reverse primer

<400> 20
acacgagctc ctacttgag gcagtcatga agct 34

<210> 21
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Forward primer

<400> 21
gtgtccatgg ctgcggggc aagtgtcggg actgaccatc atcatcatca tcatcacagc 60
caccgcgact tc 72

<210> 22
<211> 35
<212> DNA


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<213> Artificial Sequence

<220>
<223> Reverse primer

<400> 22
gtgcgatcc ctacttggag gcagtcatga agctg 35

<210> 23
<211> 16
<212> PRT
<213> Homo sapiens

<400> 23
Met Ala Arg Arg Ala Ser Val Gly Thr Asp His His His His His His
1          5          10          15

<210> 24
<211> 22
<212> PRT
<213> Artificial Sequence

<220>
<223> Peptide sequence TiP 13.40

<400> 24
Ala Tyr Arg Trp Arg Leu Ser His Arg Pro Lys Thr Gly Phe Ile Arg
1          5          10          15
Val Val Met Tyr Glu Gly
20

<210> 25
<211> 66
<212> DNA
<213> Artificial Sequence

<220>
<223> Nucleotide sequence encoding TiP13.40

<400> 25
gcgtaccgct ggcgcctgtc ccacgcgccg aaaaccggct ttatccgcgt ggtgatgtac 60
gaaggc 66

<210> 26
<211> 101
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 26
gtgtactagt gtggcgacagg cggcgtaccg ctggcgccgt tccatcgcc cgaaaaccgg 60
ctttatccgc gtggtgatgt acgaaggcta aggatccgcg c 101

<210> 27
<211> 101
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

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<400> 27
 gcgcggatcc ttagccttcg tacatcacca cgcggataaa gccggttttc gggcgatggg 60
 acagcgcca gcggtacgcc gcctgcgcca cactagtaca c 101

<210> 28
 <211> 101
 <212> PRT
 <213> Homo sapiens

<400> 28
 Met Ser Ser Ala Ala Gly Phe Cys Ala Ser Arg Pro Gly Leu Leu Phe
 1 5 10 15
 Leu Gly Leu Leu Leu Leu Pro Leu Val Val Ala Phe Ala Ser Ala Glu
 20 25 30
 Ala Glu Glu Asp Gly Asp Leu Gln Cys Leu Cys Val Lys Thr Thr Ser
 35 40 45
 Gln Val Arg Pro Arg His Ile Thr Ser Leu Glu Val Ile Lys Ala Gly
 50 55 60
 Pro His Cys Pro Thr Ala Gln Leu Ile Ala Thr Leu Lys Asn Gly Arg
 65 70 75 80
 Lys Ile Cys Leu Asp Leu Gln Ala Pro Leu Tyr Lys Lys Ile Ile Lys
 85 90 95
 Lys Leu Leu Glu Ser
 100

<210> 29
 <211> 106
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 29
 cticactagt gtggcgccagg cgaacggccg caaaatctgc ctggacctgc aggcgcgcgt 60
 gtacaaaaaa atcatcaaaa aactgctgga aagctaagga tccgcg 106

<210> 30
 <211> 106
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 30
 cgcggatcct tagctttcca gcagtttttt gatgattttt ttgtacagcg gcgcctgcag 60
 gtccaggcag attttgcggc cgttcgctcg gcgcacacta gtgaag 106

<210> 31
 <211> 85
 <212> PRT
 <213> Homo sapiens

<400> 31
 Ile Tyr Ser Phe Asp Gly Arg Asp Ile Met Thr Asp Pro Ser Trp Pro
 1 5 10 15
 Gln Lys Val Ile Trp His Gly Ser Ser Pro His Gly Val Arg Leu Val
 20 25 30
 Asp Asn Tyr Cys Glu Ala Trp Arg Thr Ala Asp Thr Ala Val Thr Gly
 35 40 45

Leu Ala Ser Pro Leu Ser Thr Gly Lys Ile Leu Asp Gln Lys Ala Tyr
 50 55 60
 Ser Cys Ala Asn Arg Leu Ile Val Leu Cys Ile Glu Asn Ser Phe Met
 65 70 75 80
 Thr Asp Ala Arg Lys
 85

<210> 32
 <211> 44
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 32
 ggcttcacta gtgtggcgca ggcgatatac tcctttgatg gtcg

44

<210> 33
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Oligonucleotide

<400> 33
 cgcgatcct tacttcctag cgtctgtcat gaaactg

37

<210> 34
 <211> 7117
 <212> DNA
 <213> E. coli

<400> 34

cccgggcact	tcgggggcat	gagtatgtga	tatccggggc	tgcaccccg	accgcccaa	60
cacatcacgg	gccacaaaat	ttttgtggc	ccgctctgcg	ttttctaagt	gttatccctc	120
ctgatttcta	aaaaatttcc	cacctgaact	tgacagaaaa	aacgatgacg	agtacttttt	180
gatctgtaca	taaacccagt	ggttttatgt	acagtattaa	tcgtgtaatc	aattgtttta	240
acgcttaaaa	gagggaattt	ttatgagcgg	tgccgatgga	cgcgccata	acacggcgcc	300
gcatagcaca	agtggttaaca	ttaatggtgg	cccgaccggg	cttggtgtag	gtgggtgtgc	360
ttctgatggc	tcgggatgga	gttcggaaaa	taaccctgtg	ggtggtggtt	ccggtagcgg	420
cattcactgg	ggtggtgtgt	ccggtcatgg	taatggcggg	gggaatggta	attccgggtg	480
tggttcggga	acaggcggta	atctgtcagc	agtagctgcg	ccagtggcat	ttggttttcc	540
ggcactttcc	actccaggag	ctggcggtct	ggcggtcagt	atttcagcgg	gagcattatc	600
ggcagctatt	gctgatatta	tggtgcccct	gaaaggaccg	tttaaatttg	gtctttgggg	660
ggtggcttta	tatggtgtat	tgccatcaca	aatagcgaaa	gatgacccca	atatgatgtc	720
aaagattgtg	acgtcattac	ccgcagatga	tattactgaa	tcacctgtca	gttcattacc	780
tctcgataag	gcaacagtaa	acgtaaatgt	tcgtgttggt	gatgatgtaa	aagacgagcg	840
acagaatatt	tcggttggtt	caggtgttcc	gatgaagtgt	ccggtggttg	atgcaaaacc	900
taccgaacgt	ccgggtgttt	ttacggcatc	aattccaggt	gcacctgttc	tgaatatttc	960
agttaataac	agtacgccag	cagtacagac	attaagccca	ggtgttacaa	ataatactga	1020
taaggatggt	cgcccggcag	gatttactca	gggtggtaat	accagggatg	cagttattcg	1080
attcccgaa	gacagcggtc	ataatgccgt	atatgtttca	gtgagtgatg	ttcttagccc	1140
tgaccaggta	aaacaacgtc	aagatgaaga	aaatcgccgt	cagcaggaat	gggatgctac	1200
gcatccggtt	gaagcggctg	agcgaaatta	tgaacgcgcg	cgtgcagagc	tgaatcaggc	1260
aaatgaagat	gttgccagaa	atcaggagcg	acaggctaaa	gctgttcagg	tttataattc	1320
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30

<210> 36
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<220>
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 <223> Forward primer
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<210> 45

<211> 45

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<223> Reverse primer

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46

<210> 47

<211> 33

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<213> Artificial Sequence

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<223> Forward primer

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<210> 48

<211> 33

<212> DNA

<213> Artificial Sequence

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<223> Reverse primer

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gaagataccc cgccgggccc gtccaccgtg ttccgccgc cg

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102

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ccagcgggcg ggaggaggtc ggccggcgaa acacggtgga cgg

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<210> 56
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 <212> DNA
 <213> Bacteriophage

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<221> modified_base
 <222> (1)...(1)
 <223> n=a, c, g, or t

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 1 5 10

aac gcg ctg cag gaa gat acc ccg ccg ggc ccg tcc acc gtg ttt cgc 96
 Asn Ala Leu Gln Glu Asp Thr Pro Pro Gly Pro Ser Thr Val Phe Arg
 15 20 25 30

ccg ccg acc tcc tcc cgc ccg ctg gaa acc ccg cat tgc cgc gaa atc 144
 Pro Pro Thr Ser Ser Arg Pro Leu Glu Thr Pro His Cys Arg Glu Ile
 35 40 45

cgc atc ggc atc gcg ggc atc acc atc acc ctg tcc ctg tgc ggc tgc 192

Arg Ile Gly Ile Ala Gly Ile Thr Ile Thr Leu Ser Leu Cys Gly Cys
50 55 60

gcg aac gcg cgc gcg ccg acc ctg cgc tcc gcg acc gcg gat aac tcc 240
Ala Asn Ala Arg Ala Pro Thr Leu Arg Ser Ala Thr Ala Asp Asn Ser
65 70 75

gaa aac acc ggc ttt aaa aac gtc ccg gat ctg cgc acc gat cag ccg 288
Glu Asn Thr Gly Phe Lys Asn Val Pro Asp Leu Arg Thr Asp Gln Pro
80 85 90

aaa ccg ccg tcc aaa aaa cgc tcc tgc gat ccg tcc gaa tat cgc gtc 336
Lys Pro Pro Ser Lys Lys Arg Ser Cys Asp Pro Ser Glu Tyr Arg Val
95 100 105 110

tcc gaa ctg aaa gaa tcc ctg atc acc acc acc ccg tcc cgc ccg cgc 384
Ser Glu Leu Lys Glu Ser Leu Ile Thr Thr Thr Pro Ser Arg Pro Arg
115 120 125

acc gcc cgc cgc tgc atc cgc ctc tgaaagcttg gctgttttgg cggatgagag 438
Thr Ala Arg Arg Cys Ile Arg Leu
130

aagattttca gctgataca gattaaatca gaacgcagaa gcggtctgat aaaacagaat 498
ttgcctggcg gcagtagcgc ggtggtccca cctgacccca tgccgaactc aga 551

<210> 58
<211> 134
<212> PRT
<213> Bacteriophage

<400> 58
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Thr Ser Ser Arg Pro Leu Glu Thr Pro His Cys Arg Glu Ile Arg Ile
35 40 45
Gly Ile Ala Gly Ile Thr Ile Thr Leu Ser Leu Cys Gly Cys Ala Asn
50 55 60
Ala Arg Ala Pro Thr Leu Arg Ser Ala Thr Ala Asp Asn Ser Glu Asn
65 70 75 80
Thr Gly Phe Lys Asn Val Pro Asp Leu Arg Thr Asp Gln Pro Lys Pro
85 90 95
Pro Ser Lys Lys Arg Ser Cys Asp Pro Ser Glu Tyr Arg Val Ser Glu
100 105 110
Leu Lys Glu Ser Leu Ile Thr Thr Thr Pro Ser Arg Pro Arg Thr Ala
115 120 125
Arg Arg Cys Ile Arg Leu
130

<210> 59
<211> 444
<212> DNA
<213> Bacteriophage

<220>
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<222> (1)...(1)
<223> n=a, c, g, or t
<221> CDS

<222> (7)...(427)

<400> 59
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cgt cag cgc cgt cgc atg aac gcg ctg cag gaa gat acc ccg ccg ggc 96
Arg Gln Arg Arg Arg Met Asn Ala Leu Gln Glu Asp Thr Pro Pro Gly
15 20 25 30
ccg tcc acc gtg ttt cgc ccg ccg acc tcc tcc cgc ccg ctg gaa acc 144
Pro Ser Thr Val Phe Arg Pro Pro Thr Ser Ser Arg Pro Leu Glu Thr
35 40 45
ccg cat tgc cgc gaa atc cgc atc ggc atc gcg ggc atc acc atc acc 192
Pro His Cys Arg Glu Ile Arg Ile Gly Ile Ala Gly Ile Thr Ile Thr
50 55 60
ctg tcc ctg tgc ggc tgc gcg aac gcg cgc gcg ccg acc ctg cgc tcc 240
Leu Ser Leu Cys Gly Cys Ala Asn Ala Arg Ala Pro Thr Leu Arg Ser
65 70 75
gcg acc gcg gat aac tcc gaa aac acc ggc ttt aaa aac gtc ccg gat 288
Ala Thr Ala Asp Asn Ser Glu Asn Thr Gly Phe Lys Asn Val Pro Asp
80 85 90
ctg cgc acc gat cag ccg aaa ccg ccg tcc aaa aaa cgc tcc tgc gat 336
Leu Arg Thr Asp Gln Pro Lys Pro Pro Ser Lys Lys Arg Ser Cys Asp
95 100 105 110
ccg tcc gaa tat cgc gtc tcc gaa ctg aaa gaa tcc ctg atc acc acc 384
Pro Ser Glu Tyr Arg Val Ser Glu Leu Lys Glu Ser Leu Ile Thr Thr
115 120 125
acc ccg tcc cgc ccg cgc acc gcc cgc cgc tgc atc cgc ctc t 427
Thr Pro Ser Arg Pro Arg Thr Ala Arg Arg Cys Ile Arg Leu
130 135 140
gaaagcttgg ctgtttt 444

<210> 60

<211> 140

<212> PRT

<213> Bacteriophage

<400> 60

Met Ala His His His His His Tyr Gly Arg Lys Lys Arg Arg Gln
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Thr Val Phe Arg Pro Pro Thr Ser Ser Arg Pro Leu Glu Thr Pro His
35 40 45
Cys Arg Glu Ile Arg Ile Gly Ile Ala Gly Ile Thr Ile Thr Leu Ser
50 55 60
Leu Cys Gly Cys Ala Asn Ala Arg Ala Pro Thr Leu Arg Ser Ala Thr
65 70 75 80
Ala Asp Asn Ser Glu Asn Thr Gly Phe Lys Asn Val Pro Asp Leu Arg
85 90 95
Thr Asp Gln Pro Lys Pro Pro Ser Lys Lys Arg Ser Cys Asp Pro Ser
100 105 110

Glu Tyr Arg Val Ser Glu Leu Lys Glu Ser Leu Ile Thr Thr Thr Pro
 115 120 125
 Ser Arg Pro Arg Thr Ala Arg Arg Cys Ile Arg Leu
 130 135 140

<210> 61
 <211> 1565
 <212> DNA
 <213> Salmonella

<400> 61
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